

IN THE SPECIFICATION:

Please replace Paragraph No. 00055 with the following paragraph:

-- The present invention provides purified and isolated polynucleotides (*e.g.*, DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single- and double-stranded, including splice variants thereof) that encode unknown G protein-coupled receptors heretofore termed novel GPCRs, or nGPCRs. Table 1 below identifies the SEQ ID NO: of the gene sequence, the SEQ ID NO: of the polypeptide encoded thereby, and the U.S. Provisional Application in which the gene sequence has been disclosed.

Table 1

nGPCR	Nucleotide Sequence (SEQ ID NO:)	Amino acid Sequence (SEQ ID NO:)	Originally filed in:
2037	1	2, 3	A, B

Legend

A= Ser. No. 60/195,228

B= Ser. No. 60/251,313

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Please replace Paragraph No. 00117 with the following paragraph:

-- Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table 2 (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

Table 2
Conservative Substitutions I

<u>SIDE CHAIN</u> <u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	
Non-polar	G A P I L V
Polar - uncharged	C S T M N Q
Polar - charged	D E K R
Aromatic	H F W Y
Other	N Q D E

Please replace Paragraph No. 00118 with the following paragraph:

-- Alternatively, conservative amino acids can be grouped as described in Lehninger, (*Biochemistry*, Second Edition; Worth Publishers, Inc. NY, NY (1975), pp.71-77) as set out in Table 3, below.

Table 3
Conservative Substitutions II

<u>SIDE CHAIN</u> <u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Non-polar (hydrophobic)	
A. Aliphatic:	A L I V P
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	S T Y
B. Amides:	N Q
C. Sulfhydryl:	C
D. Borderline:	G
Positively Charged (Basic):	K R H
Negatively Charged (Acidic):	D E

Please replace Paragraph No. 00119 with the following paragraph:

-- As still another alternative, exemplary conservative substitutions are set out in Table 4, below.

Table 4
Conservative Substitutions III

Original Residue	Exemplary Substitution
Ala (A)	Val, Leu, Ile
Arg (R)	Lys, Gln, Asn
Asn (N)	Gln, His, Lys, Arg
Asp (D)	Glu
Cys (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
His (H)	Asn, Gln, Lys, Arg
Ile (I)	Leu, Val, Met, Ala, Phe.
Leu (L)	Ile, Val, Met, Ala, Phe
Lys (K)	Arg, Gln, Asn

Met (M)	Leu, Phe, Ile
Phe (F)	Leu, Val, Ile, Ala
Pro (P)	Gly
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser
Val (V)	Ile, Leu, Met, Phe, Ala

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Please replace Paragraph No. 00236 with the following paragraph:

-- The following Table 5 contains the sequences of the polynucleotides and polypeptides of the invention. The transmembrane domains within the polypeptide sequence are identified by underlining.

Table 5

The following DNA sequence nGPCR-2037 <SEQ ID NO. 1> was identified in *H. sapiens*:

TGAAGTACGGCGAGGCGTAAAGACAAACCTAATAAGAAATCTAACTCTCTTAAATTTTAA
 AATATGCTGTGTGATGCTGCTTTTCAGAGCTCTAACTCCAGCAGCATGAATGTGTGCTTTTAA
 GCTTAACTTTCGGGAGGGTACCTGCCCTCTGATTCCCAGGACTGGAGAACCATTATCCCGGCT
 CTCTCTTTGGCTGTCTGCTGGTGGGCTTCGTGGGAAACCTGTGTGTGATTGGCATGCTGCTT
 AATATGCTTGAAGGAAGCCATCCATGATCCACTGCTGATTCTGAATCTGAATTTGGCTGA
 TGTCTCTTCTCTGCTTTTCTGCACCTATCCAGCTACGGGCTACTCCAAAATTTTGGAT
 TTAATCTGCTTTTCTCTGAAGTCTCTGACTGCTTTATCCACACATGCATGGAAATTAAGCT
 TTAATCTGCTTCTCTTAAATATATCTGCTTATTAAGTATCCATTTAAATTAATTAAT
 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

The following amino acid sequences <SEQ ID NOS. 2 and 3> are predicted amino acid sequences derived from the DNA sequence of SEQ ID NO. 1:

MIAAFAEENWNNVSEFHLHFAGGYLPOLSQEWRTIIPALLVAVCLVGFVGNLCVIGILLHWAFWFKK
 WNLILNLSLADLSLLLFSAPIRATAYSKQVWDLQWFWVSSDWFIHTCMAAKSLTIVVAVKVCIFYACDPA
 PLYLHNYTIWSVLVAIWTVASLLPLEWFFESTIPHHGEMCLWDVPAVAEEFMSMFPLYLLAFLGLPLF
FASFYFWAYTQCKKRGTYQNLENQIRSKQVTWLLSIAIISALLWLPEWWAWLWWHLMAAGASFGFI
ALSQVLMFSISSANPLIFLWSEEFREGLKGVWWMITKYPPTVSESQETPAGNSEGLETFWSPFACIP
 EYALIANWFWPTXAEIPLPLVEQFWHRTITVGVQNSDFPWHEHSDQETGEGWY

SEQ. ID. NO. 1

ENHFAHLEHFAEYLICLQDWRTHIPALLVAVCLVGFVGNLCVIGILLHNAWKGKIKTHLILNLSLADL
SLLFSAPIRATAYKSTADLEWFCVKSCLWFIHTCMAAKSLTIVVAKVCFMYASLPANVTHNYTIWSV
LVAIWTVASLLPLPEWFEETIPHHHEGVEMCLVDVFAVAEEFMSMFGYLYPLLAFGPLFFASFYFWAYLQV
RHPVHTYTHNENQIRKLVTVLLSIAIISALLWLPEWVAWLWVWHLKAAGFAPKGFIALSQVLMESISSA
NPLIFLWVDEEFREGLYGVWWMITKYPPTVCEQGETPAGNSEGLPDKVPSPESPANDEPEKESPEQKQK
KTEHARIPILLIVEQFWHERDTVPSVQDNDPIPEWEHELQETGEGVK

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